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Economical Productivity of Maize Genotypes under Different Herbicides Application in Two Contrasting Climatic Conditions

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Abstract: Maize ranks first among worldwide production and an important source of human and animal feed. Its production can be affected by management practices and climatic conditions. The objective of this study was to estimate stability of yield and hundred grains weight of six maize genotypes during two growing seasons at two locations, subjected to four different treatments: T_1 treatment—without herbicide, Control; T_2 treatment—active substance Nicosulfuron and Motivell commercial preparation; T_3 treatment—active substance Rimsulfuron and Tarot; and, T_4 treatment—active substance Forasulfuron and Equip. Additive main effects and multiplicative interaction—AMMI model and genotype × environment interaction—GGE biplot were used to estimate GEI—genotype by environment interaction. The results showed that the influence of genotype (G), year (Y), locality (L), treatment (T) and all interaction on hundred grains weight were significant. The share of genotypes in the total phenotypic variance was 64.70%, while the share in total interaction was 26.88%. The share of IPCA1 in terms of G × T interaction was 50.6%, while share of IPCA2 was 44.74%, which comprised together 94.80% of interaction. The first IPCA1 axis showed high share in the total interaction, which indicates out significance of genotype in total variation and interaction, while high level of IPCA2 indicates a significant treatment effect. Genotype L-6 had the same mass of 100 grains (37.96 g) during both years of testing, while genotype L-1, with 4.46 g, had the largest difference between years. This clearly indicates the influence of genotype but also stress under the influence of sulfonylureas and environmental factors. The maize genotype with the highest values of hundred grains weight, L-5 and L-6, expressed the highest values of grain yield (4665 kg ha^{-1} and 4445 kg ha^{-1}).

Keywords: *Zea mays*; genotype; principal components analysis-PCA; grain yield component; stability

1. Introduction

Maize (*Zea mays* L.) with wheat and rice provides food for more than 4.5 billion people in hundreds of developing countries. Maize production is an important position in the world economy; it is affected by abiotic and biotic stresses, soil fertility, quality seed and fertilizers, levels of mechanization, and post-harvest management [1,2]. It ranks third in the world in terms of distribution (143 million ha), in front of which are wheat (215 million ha) and rice (151 million ha), while in Serbia it ranks first [3–5]. Maize was

grown in Serbia in 2020 on 996,527 ha, with an average yield of 7.9 t ha^{-1} and production of 7.88 million tons. Maize is the most exported good from Serbia. In 2020, Serbia exported 16.86 million tons of maize, the value of which was 644.61 million dollars [6,7]. Maize is the preferred staple food for 900 million poor, globally, due to the large number of health benefits it offers. It is rich in: fiber, antioxidants and other vitamins and minerals [8]. New innovations and trends in the areas of genomics, bioinformatics, and phenomics are enabling breeders with innovative tools, resources and technologies to breed superior resilient cultivars. Maize breeding strategies create highly yielding and adaptable genotypes for different production environments [9]. In order to create maize hybrids for wide production, aside from the genetic potential for high yield, this requires good adaptability and stability, quick moisture release from the grain and good resistance to economically significant pests and plant diseases. Therefore, in maize breeding programs, besides the appropriate germplasm, it is necessary to apply adequate breeding methods that will ensure the implementation of the program in the shortest possible time and low possible cost [8,9]. Genotype is one of the very important factors of cultivation that can be influenced [10–13]. The various genotype traits in different conditions are due to its genetic structure, but also require knowledge about the yield components, their relationship and their stability [14]. Given that grain yield as a complex trait includes many quantitative components and has a polygenic inheritance, breeders normally use yield components to improve the grain yield, despite the fact that these components compensate each other in practice, and an increase in one causes a decrease in the other component [15,16]. Grain yield and hundred grains weight (g) are the important parameters for estimating maize genotype value, in breeding programs of standard grain quality maize. As maize plants grow, so does the photosynthesis of the plant and its greater ability to transport assimilates of organs used for different uses [17,18]. The phenotype is formed on the basis of the capacity of its genotype under the influence of environmental factors [19–22]. Results of multi-environment trials have demonstrated the existence of genotype by environment interaction [23]. Differential genotypic responses to different environments are collectively called genotype by environment interaction (GEI) and represent permanent interest for breeders, geneticists and biometricians with its practical and theoretical aspects [10,24,25]. The presence of a significant GEI complicates the selection of superior cultivars and the best testing sites for identifying superior and stable maize genotypes [26]. Given regionalization or cultivation of varieties in different agroecological conditions, the most productive and stable varieties can be determined [27,28]. Since it can lead to gains or losses in breeding programs, GEI in breeding programs has recently received considerable attention through the use of field tests set up in different locations [29,30]. By applying appropriate statistical methods, it is possible to exclude the consequences of the GEI and environmental, external factor and select stable and high-yielding maize genotypes. The most commonly used statistical analysis for the interpretation of GEI is based on the use of biplots of the Additive main effects and multiplicative interaction (AMMI) model. The AMMI model is ordinarily the model of choice when the main effects and interaction are both important, which is the most common case with yield trials [31–33]. This model is distinguished because it interprets the effects of genotype (G) and the location (E) as additive, and on the GEI, as a multiplicative non-additive component. The model combines firstly the analysis of variance (ANOVA) to partition the variation into genotype main effects (G), environment main effects (E) and GEI effects and then applies principal components analysis (PCA) to GEI in a single analysis [34]. However, the GGE biplot method, being near to the AMMI analysis on the basis of which the main components of genotypes and environments, i.e., interactions, were obtained [35–39].

Maize is a very important raw material for the processing industry, because it contains carbohydrates, proteins, fiber, minerals and other nutrients [11,40] (Table 1). Maize is rich in carbohydrates and low in fat, so it is a good source of quickly available energy. Whether we use corn as a grain, vegetables or snacks, we fill the body with energy, protect ourselves from viruses, and contribute to heart health and blood vessels. The maize grain has the largest germ which contains a large percentage of fat and sugar. High quality oil is produced from sprouts, it is rich in vitamins A, C and E (fertility vitamin) and unsaturated fatty acids. The oil is recommended as a medicine code progressive senile atherosclerosis because it lowers cholesterol levels. It is enough to use 20 g of oil daily as a supplement to the regular diet. Maize grain contains: Calories 342.5; Energy 1399.1 K; Moisture 15.0 g; Carbohydrates 66.3 g; Protein 10.3 g; Lipid 3.7 g; Ash 1.6 g; Fibre 2.8%; Sugars 1.7 g; Minerals: 1.6 mg; Phosphorus 348.3 mg; Sulphur 114.0 mg; Calcium 10.3 mg; Iron 2.5 mg; Potassium 286.2 mg; Magnesium 139.1 mg; Copper 0.15 mg; Amino Acids 1.79 mg; Riboflavin 0.14 mg; Thiamine 0.43 mg; Folates 39.4 mg, Carotene 90.2 mg, Table 1.

Table 1. Nutritional composition of grain maize.

Parameters	Quality Contents	Minerals	Content
Calories	342.0	Calcium (Ca, mg)	10.0
Energy (K)	1399.1	Zinc (Zn, mg)	5.0
Moisture (g)	14.9	Iron (Fe, mg)	2.3
Carbohydrates (g)	66.2	Potasium (K, mg)	286.0
Protein (g)	11.1	Magnesium (Mg, mg)	139.0
Lipid (g)	3.6	Copper (Cu, mg)	0.14
Fibre (g)	2.7	Carotene (A, mg)	90.0
Ash (g)	1.6	Folates (B9, mg)	39.4
Total free sugars (g)	1.7	Niacin (B3, mg)	2.2
Minerals (mg)	1.5	Riboflavin (B2, mg)	0.20
Phosforus (P, mg)	348.0	Thiamine (B1, mg)	0.42
Sodium (Na, mg)	15.9	Pantothenic Acids (B5, mg)	0.3
Amino Acids (mg)	1.8	Pyridoxine (B6, mg)	0.3
Sulphur (S, mg)	114.0	Ascorbic acid (C, mg)	0.12

Therefore, the objective of this research was to determine the influence of genotype, year, locality of cultivation and treatment, with four herbicide sub-treatments, on the stability [41,42] of yield component, hundred grains weight (g) of six tested maize genotypes by using the AMMI and GGE biplot methods. The information obtained through this investigation would be beneficial to maize producers, as well as breeders, to select the appropriate suitable and stable maize hybrids that can be successfully exploited in different environments based on genotype stability, without additional requirements for developing breeding programs for smaller and specific environments.

2. Materials and Methods

2.1. Field Emergence

Six maize genotypes were tested in this study, namely, L-1 to L-6, during two successive growing seasons of 2017 and 2018. The investigation was carried out at the two localities, in Zemun Polje (Locality 1) and in Pancevo (Locality 2), in Serbia. The experiment was performed in four variants and three replicates according to the randomized complete block design (RCBD). Before plowing, basic fertilization with mineral nutrients was performed using formulations NPK 15:15:15 in the amount of 350 kg ha^{-1}. Each maize genotype was planted in four rows, hence each experimental plot contains 4 rows (2.8 m^2 wide) and is 15 m long. The density of crops was 74,280 plants per hectare. In the field trial, standard maize cultivation technology was applied except for variants with treatment, while harvesting was done manually. The experiments were subjected with four herbicide sub-treatments: 1. Treatment–control, treatment was done with water without herbicide (T$_1$); 2. Treatment–active substance, Nicosulfuron and the Motivell commercial preparation

in the amount of 1.25 L ha^{-1} (6.3 mL per treatment) applied (T$_2$); 3. Treatment–active substance Rimsulfuron and the Tarot commercial preparation in the amount of 60 g ha^{-1} (0.3 g per treatment) (T$_3$); 4. Treatment–Active substance Forasulfuron and the Equip commercial preparation in the amount of 2.5 L ha^{-1} (12.6 mL per treatment) (T$_4$). Each plot area for herbicide treatment and for control plot was 50 m^2. Herbicides were applied in the stage of V9–V10 (9–10 developed leaves) and 15–16 BBCH scale of maize. Herbicides were applied with a Solo spiral type with Tee Jet KSR11003 and water consumption of 250 L ha^{-1}, in order to obtain data on the following grain yield traits at the technological maturity 10 plants from each genotype and replications [3,4,35]. Biometric data processing is based on repetition for grain yield. Data regarding hundred grains weight (g) was recorded by counting actual number of hundred grains at random and then weight was measured.

2.2. Meteorological Data

Average monthly temperature was 18.4 °C in the first year and 19.5 °C in the second year, in the Pancevo locality (Figure 1a).
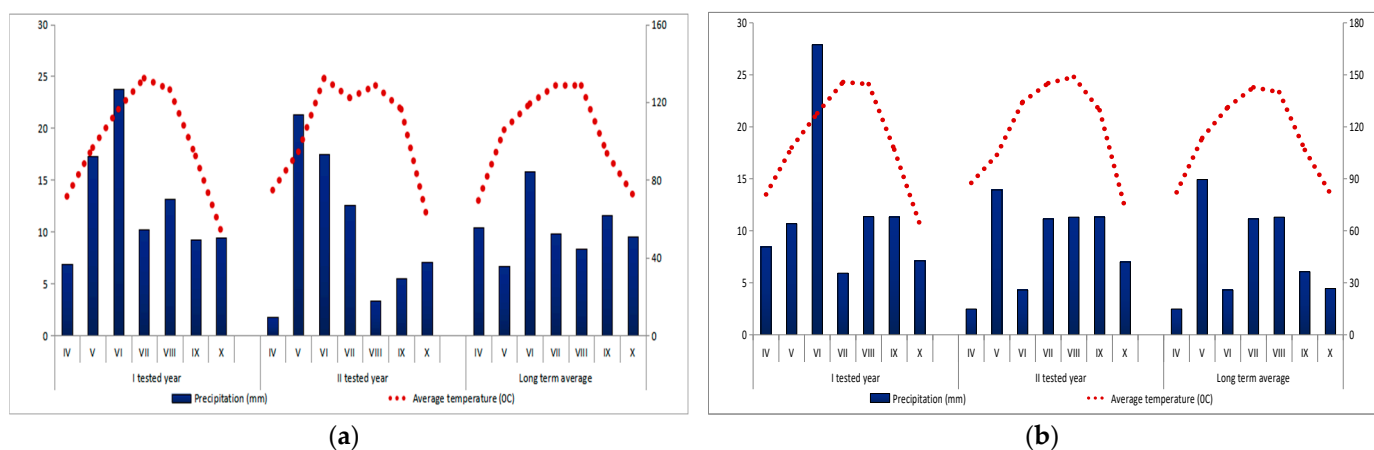

(**a**)
(**b**)

Figure 1. Average temperature (°C) and total precipitation (mm) during two maize growing seasons in both the locality in Pancevo (**a**) and in Zemun Polje, Serbia (**b**).

The average monthly temperature in the locality Zemun Polje was 18.5 °C in the 2010 growing season and 19.6 °C in the growing season of 2011 (Figure 1a). Total precipitation in the vegetation period maize amounted to 480 mm in the first year and 369 mm in the second year in the first locality, in Pancevo. Total precipitation in the locality o Zemun Polje as 497 mm in the first growing season and 328 mm in the second growing season. In the second growing season, it was recorded a deficit of precipitation of optimum for 99 mm (Pancevo) and 150 mm (Zemun Polje), Figure 1b. All meteorological data, average values of temperature and total monthly precipitation throughout the seasons were accessed through the weather stations in Pancevo and Zemun Polje, in Serbia.

2.3. Statistical Analysis

In order to estimate phenotypic variability, the influence of genotypes, environments and genotype by environment interaction, the AMMI (Additive Main Effect and Multiplicative Interaction) model was used and represented by the following formula [43]:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \Sigma_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger}$$

where Y$_{ger}$ is the yield for the genotype g in the environment e the replication r. The additive parameters are: m—the grand mean, α_g—a/the genotypic mean deviation from the grand mean, β_e—the environmental mean deviation. The multiplicative parameters are: λ_n— a singular value for n interaction principal component axis n, γ_{gn}—the genotype eigen vector for IPCA axis n, δ_{en}—the eigen vector of the environment for IPCA axis n, ρ_{ge}—

a residue when not all PCA axis are included and e_{ger}—the error. The AMMI model incorporates analysis of variance (ANOVA) and principal components analysis (PCA) in a single statistical model [29,37,43].

Statistical data analysis was performed using the GenStat 12th computer statistical program (GenStat for Windows 12th Edition, VSN International, Hemel Hempstead, Wood Lane, London, UK). AMMI analyses were also performed in Excel Biplot Macros. Among multivariate analysis models, the additive main effects and multiplicative interaction (AMMI) biplot and the genotype main effect and genotype × environment interaction (GGE) biplot have been frequently used to visualize G × E interaction. In the AMMI model, using ANOVA additive effects is separated from interaction effects, while additional GEI analysis can be done by Principle Component Analysis (PCA) [10,36,38,41,44].

In order to further evaluation of maize genotypes and localities, as well as genotypes and treatments, GGE biplot analysis was applied according to [41]:

$$\hat{Y}ij = \mu + \alpha i + \beta j + \Phi ij$$

where $\hat{Y}_{ij}$—presents expected yield genotype *i* in environment conditions *j*, μ—mean value each observations, α*i*—the genotype effect *i*, β*j*—environment effect *j*, Φ*ij*—interaction genotype *i* and environment. Such genotypes are characterized by broad adaptability, in contrast to genotypes of specific adaptability, which are located far from the coordinate origin. The characteristic of the GGE biplot method is that, when studying the stability of the yield, it jointly analyzes the variability caused by the genotype and the genotype–environment interaction, dividing it into two parts:

$$\hat{Y}_{ij} - \mu - \beta_j = gi1e1j + gi2e2j + \Sigma_{ij}$$

where *gi1* and *e1j* present primary genotype *i* and locality *j* estimation, while *gi2* and *e2j* present secondary estimation for genotype *i* and locality *j* and Σ_{ij} present unexplained residue. The GGE biplot is constructed by plotting the first principal component (PC1) scores of the genotypes and the environments against their respective scores for the second principal component (PC2) that result from singular value decomposition of environment-centered or standardized genotype by environment data [39,41]. GGE biplot is an effective tool for: (1) mega-environment analysis (e.g., "which-won-where" pattern), while specific genotypes can be recommended to specific mega-environments analysis [39,41], (2) genotype evaluation based on the mean performance and stability, and (3) environmental evaluation based on the power to discriminate among genotypes in target environments [35,39,41]. In GGE biplot genotypes with a high value of the PC1, the component possesses high average values for the yield of grain and its component. At the same time, the genotypes with high values of components of PC1 and PC2 values of the components are close to zero, representing the genotypes of interest for further investigations.

3. Results

Maize grain yield and hundred grains weight of maize are among the most important maize breeding parameters. For yield estimation, it is important to determine genetic control grain mass and other yield traits, as well as investigation of the influence of environmental factors and effects of genotype × environment interaction [43]. Potential yield refers to the maximum yield that can be attained by a crop in a given environment [11,42]. However, genotype reaction for grain weight parameters in interaction makes phenotypic expression for this trait more difficult to predict.

3.1. Mean Values of Grain Yield of Maize

In the present study, maize genotypes showed relation between traits of hundred grains weight and grain yield. The maize genotype with the highest values of hundred grains weight, L-5 (38.06 ± 3.07 g) and L-6 (37.58 ± 2.41 g), expressed the highest values of grain yield (4665 ± 315.00 kg/ha and 4445 ± 337.00 kg/ha). Increasing one hundred grains weight also increased grain yield of maize genotypes. Maize genotypes with the lowest grain yield, L-2 (2764 ± 680.00 kg/ha) and L-1 (2910 ± 493.00 kg/ha), expressed the lowest value of hundred grains weight (24.63 ± 7.65 g and 25.42 ± 7.70 g). As shown in Table 1, the genotypes L-2 (24.16%) and L-1 (18.26%) have the bigger coefficient of variation for the grain yield, while the lowest variations were observed for genotypes L-5 (7.11%) and L-6 (8.11%), while moderate variations were found for maize genotypes L-3 (12.66%) and L-4 (13.85%). In the second year, there was a deficit of precipitation of optimum, for 99 mm (Pancevo) and 150 mm (Zemun Polje), which caused a decrease in yield compared to the first year.

High-yielding genotypes, suitable for intensive growing conditions, in optimal conditions achieve results close to the genetic potential for grain yield. However, in areas and years with less favorable conditions, a decline in the achieved maize grain yield is evident. Bozović et al. [3] explain that highly statistically significant differences in average yield values between years are expected and justified, and that they indicate the great influence of climatic factors during vegetation on grain yield height formation, which confirms the importance of genotype–location interaction and clearly indicates the variability of yield under the influence of the environment.

This finding further confirms the results of previous research, which reported that variation in grain weight can have a large impact on the final yield of maize [44–46]. Obtained result is not common in practice, but it indicates that increasing of genetic potential of grain yield is possible to achieve through increasing the size and capacity of grain. Yield is usually in a negative correlation with quality, which represents the main difficulties in efficient breeding and developing enhanced cultivars with improved and stable grain yield [41,47]. In addition, an increase in plant density could lead to smaller mass of individual dry matter in plants, which may have contributed to the smaller mass of grains, due to a reduced supply of photo-assimilates to developing grains [48]. According to Serpa et al. [49], reducing the weight of one hundred maize grains can be achieved by increasing the number of plants per unit area, which increases their competition with each other.

3.2. Mean Values of Hundred Grains Weight and Interaction IPCA1 and IPCA2

In the present study, six maize genotypes were used and average values for grain yield and hundred grains weight in different environments are presented in Table 2. The greatest overall mean value for the trait hundred grains weight in both seasons was denoted for maize genotype L-5 (38.06 ± 3.07 g), followed with genotypes L-6 (37.58 ± 2.41 g) and L-4 (36.19 ± 4.37 g) on an overall basis. Minimum values were achieved for maize genotype L-2 (24.63 ± 7.65 g) and L-1 (25.42 ± 7.70 g), whereas the average mean value was observed for genotype L-3 (31.35 ± 8.83 g). A high coefficient of variation for the trait hundred grains weight of maize was observed for the genotypes L-2 (22.58%) and L-1 (18.31%), while the lowest variation was observed for genotypes L-6 (7.17%) and L-5 (8.64%) on an overall basis, Table 1. Higher variability observed in maize genotypes L-2, L-1 and L-3 indicates the influence of the environmental conditions in which maize trials were performed, while lower values of coefficient of variation observed in genotypes L-5 and L-6 indicate that the variability was caused by variability of genetic materials through increased stability of this maize genotype in the specific environmental conditions.

Table 2. Mean values of the trait hundred grains weight (g), grain yield (kg/ha) with Standard Devijation and the interaction IPCA1 and and IPCA2 values of the AMMI model for the trait hundred grains weight (g) of six examined maize genotypes on overall bases, both seasons, localities and treatments.

| G * | HGW Mean | HGW CV(%) | Interactions | | | | | | GY (kg ha⁻¹) | GY CV (%) |
| | | | G × Y | | G × L | | G × T | | | |
			IPCAg1	IPCAg2	IPCAg1	IPCAg2	IPCAg1	IPCAg2		
L-1	25.42 (7.70)	18.31	0.338	0.000	−0.778	0.000	1.287	0.781	2910 (493)	18.26
L-2	24.63 (7.65)	22.58	0.338	0.000	−1.366	0.000	0.649	−0.558	2764 (680)	24.16
L-3	31.35 (8.83)	12.42	0.655	0.000	0.503	0.000	−0.301	−1.463	3830 (462)	12.66
L-4	36.19 (4.37)	11.95	−0.835	0.000	0.061	0.000	−0.830	0.174	4345 (602)	13.85
L-5	38.06 (3.07)	8.64	0.469	0.000	0.915	0.000	−1.099	0.898	4665 (315)	7.11
L-6	37.58 (2.41)	7.17	−0.965	0.000	0.665	0.000	0.295	0.168	4445 (337)	8.11

* G—genotypes; HGW: hundred grains weight (g); CV—coefficient of variation; GY—grain yield; G × Y—Genotype × Year interaction; G × Y—Genotype × Locality interaction; G × T—Genotype × Treatment interaction; IPCA1—The first interaction principal components axes; IPCA2—The second interaction principal components axes.

3.3. Analysis of Variance-ANOVA for Hundred Grains Weight of Maize (g)

The combined analysis of variance (ANOVA), for the trait hundred grains weight, separates the overall variability on the main-additive effects of environment (E), genotype (G) and non-additive G × E interaction, Table 3.

Calibration aims to uniform maize seeds by physical properties (mass and shape). For this purpose, different sieves are used, with round and rectangular openings, which divide maize seeds into two, three or four fractions. Using a maize seed sieve, the fraction with the highest HGW can be separated. Within the same seed dimension, it is possible to separate the seeds by weight, using gravity separators, which practically determines its seed quality [11].

The results of ANOVA for the six examined maize genotypes showed that genotype main effect (G), year (Y), location (L) and treatment (T), as well as all examined interactions (G × L, G × T, G × Y, L × T, Y × L, G × Y × L, G × Y × T, G × L × T, Y × L × T and G × Y × L × T), were all highly significant ($p < 0.001$) for the 100 grains weight (Table 2). The results showed that the largest share in the trial variation had sum of squares of years, which was higher than sum of squares of both localities and treatments. The genotype share in the total phenotypic variance for 100 grains weight was 64.70%. The cumulative share of the year, localities and treatment was 8.42%, while the share of total interaction was 26.88% (Table 2). The sum of the squares of genotypes was about seven times larger than the sum of the squares of localities, years and treatments, together indicating the importance of this source of variation. These results indicated that there was a significant difference between the genotypes reaction to the different conditions in the experiment. Maize genotypes reacted differently to the environmental factors, which caused a high sum of the squares of individual interactions, as well as high participation of interactions in the overall variation of the observed trait.

The large sum of squares of genotypes in the total trial variation indicates a large genetic divergence between that observed in genotypes for this trait. Although the usual proportion of the genotype × locality interaction counts for around 10% of the total sum of treatments in standard multi-environmental trials [50], in some cases, it can be much larger [25,51]. Table 1 shows that the components IPCA1 and IPCA2 together influenced 95% of the variations in the G × T interaction. According to the IPCAg1 values in the G × Y

interaction, the genotypes L-6 and L-4 can be characterized as low stability genotypes, with a high level of average value of hundred grains weight. Genotypes L-1 and L-2 were shown as the most stable with the lowest mean values of 100 grains weight. Based on the results of the first components in the interaction G × L, genotype L-4 can be considered as the most stable genotype, while L-2 was shown as the least stable of the maize genotypes. The results showed that genotypes that exposed a lower stability have a significantly higher average of hundred grains weight. These results suggest that these genotypes have specific additional requirements for adaptation and can be used as a measure for successful cultivation on areas within specific environments. Based on G × T interaction and according to IPCAg1, the most stable shown was the genotype L-6, while the least stable was genotype L-1 (Table 2).

Table 3. The AMMI analysis of variance for hundred grains weight (g) of six maize genotypes.

Sources of Variation *	DF	SS	SS (%)	MS
Genotype (G)	5	8801.20	64.70	1760.21 **
Year (Y)	1	609.60	4.39	609.60 **
Location (L)	1	437.60	3.02	437.60 **
Treatment (T)	3	145.00	1.07	48.33 **
G × Y	5	150.60	1.01	30.12 **
IPCA1	5	150.60	100.00	30.12 **
IPCA2	3	0.00	0.00	0.00
G × L	5	385.40	2.74	77.10 **
IPCA1	5	385.40	100.00	77.10 **
IPCA2	3	0.00	0.00	0.00
G × T	15	413.50	3.04	27.62 **
IPCA1	7	207.00	50.06	29.57
IPCA2	5	185.00	44.74	37.00
Y × L	7	207.00	1.32	29.57 **
Y × T	3	64.70	0.29	21.60 **
L × T	3	154.40	1.04	51.50 **
G × Y × L	5	145.20	1.07	29.01 **
G × Y × T	15	216.20	1.39	14.40 **
G × L × T	15	256.70	1.69	17.12 **
Y × L × T	3	211.90	1.36	70.64 **
G × Y × L × T	15	403.60	2.77	26.91 **
Error	192	1236.00	9.10	6.42
Sum	287	13,581.90	100.00	

* All sources were tested in relation to the error; **: Highly significant at $p < 0.01$ probability level; ns: not significant; DF: Degree of freedom; F: F value calculated; IPCA1: The first interaction principal components axes; IPCA2: The second interaction principal components axes.

3.4. Stability of Hundred Grains Weight of Maize

Stability for the hundred grains weight in tested maize genotypes, observed by location, can be seen in Figure 1. Maize genotypes L-6, L-5 and L-4 showed the greatest expression and high stability for hundred grains weight (Figure 2a). These genotypes achieved the level of expression and stability at the first locality. The maize genotype L-3 showed average expression and high stability, while genotypes L-2 and L-1 were shown as less important for further selection in terms of the observed trait, since they have below-average expression regardless of stability. The genotypes L-4, L-5 and L-6 had the best expression and were distinguished with high stability for the trait hundred grains weight (Figure 2b).
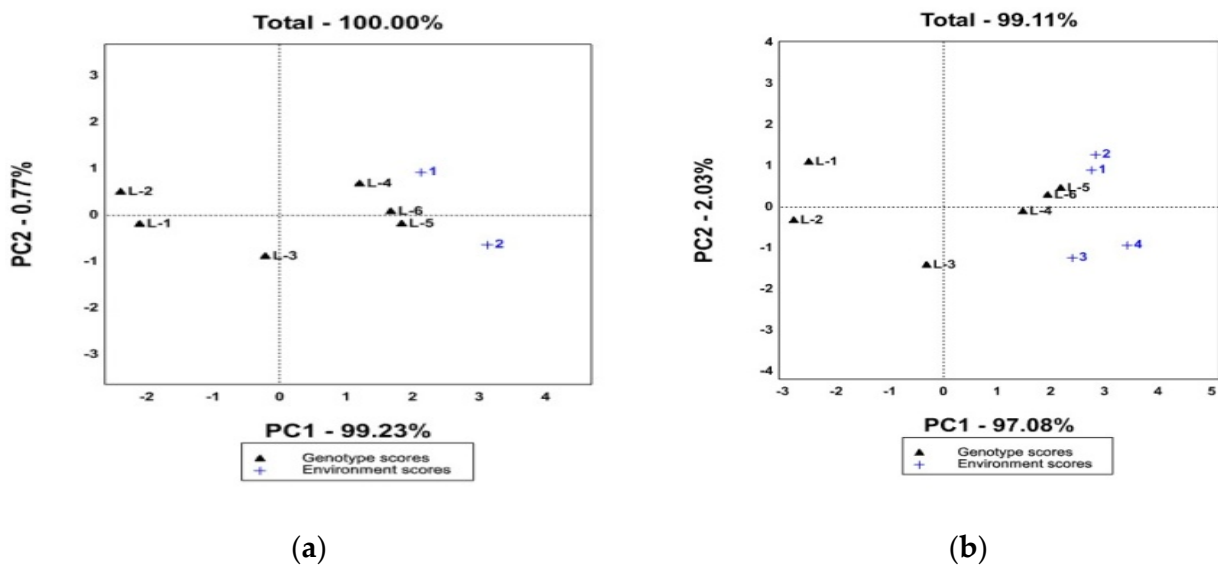
(**a**)　　　　　　　　　　　　　　　　　(**b**)

Figure 2. GGE biplot view of stability of the expression for the hundred grains weight (g) of maize genotypes based on the locality (**a**) and GGE biplot view of stability of the expression for the hundred grains weight (g) of six maize genotypes based on the treatments (**b**).

3.5. Stability of Hundred Grains Weight of Maize by Model "Which-Won-Where"

Figure 3a shows that the axes from the coordinate start split the biplot into six sectors. Both localities belong to the same sector. The most appropriate expression in the first and second locality had genotypes L-6, L-5 and L-4. As the value of locality 2 is in the same sector, the phenotypic expression of the mentioned genotypes was high in both localities.
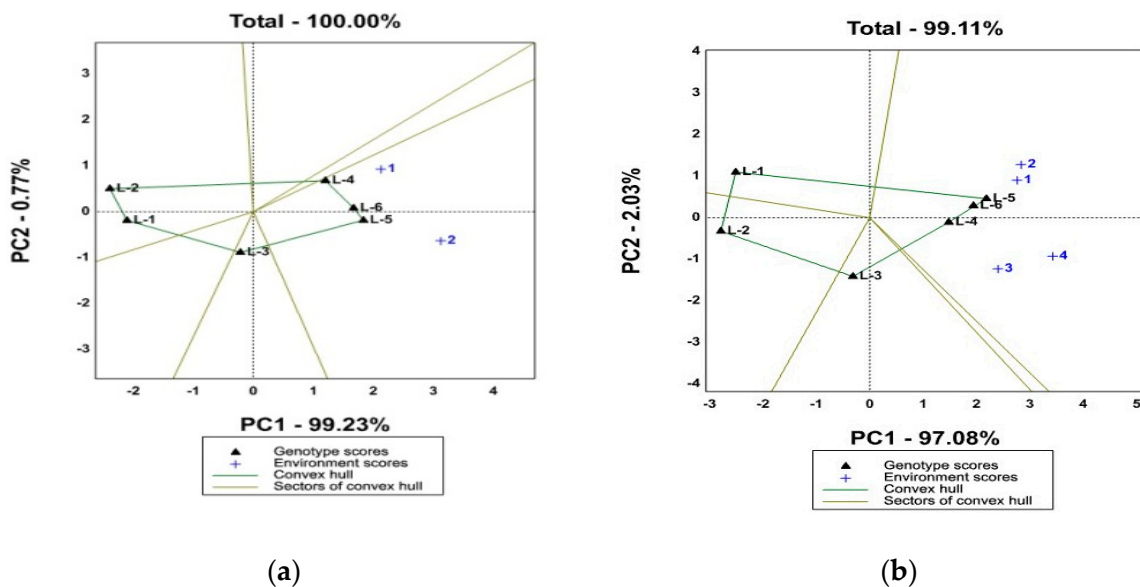

(**a**)　　　　　　　　　　　　　　　　　(**b**)

Figure 3. The "which-won-where" view of the GGE biplot view for the hundred grains weight (g) of maize genotypes based on locality (**a**) and the "which-won-where" view of the GGE biplot for thousand grains weight (g) of maize lines based on treatment (**b**).

This indicates the existence of a useful genetic variation that could be utilized in breeding programs targeted for the examined environment. The other three genotypes did not show satisfactory results in any of the observed sites, which can be explained by the fact that the observed trait of these genotypes is very variable and can be considered as very unstable in terms of both localities.

In Figure 3b, it can be seen that the axes from the coordinate start split a biplot in five sectors. All treatments belong to the same sector. Based on the phenotypic expression shown for hundred grains weight, the genotypes L-5, L-4 and L-6 occupied the same sector on the biplot. The best expression in the first, third and fourth treatment was achieved by genotypes L-6, L-5 and L-4. The other three genotypes did not show a good response in any of the applied treatments.

3.6. GGE Biplot Display of Hundred Grains Weight According to the Ideal Genotype Model Based on the Locality

The ideal genotype position is represented by the smallest circle and arrow within it and is defined by the average values of PC1 and PC2 of all localities. These are the L-4, L-5 and L-6 genotypes that achieved the best expression of the trait in both locations. The other examined genotypes were far from ideal in terms of expression of the given trait and stability. Thus, they may not be promising across these environments (Figure 4a).

In the biplot analysis of applied treatments, the same genotypes occupied the smallest arc with the arrow and were the closest to the ideal genotype, both in terms of stability and in terms of expression, while the other genotypes were far from ideal both in terms of expressing the given trait and stability (Figure 4b).
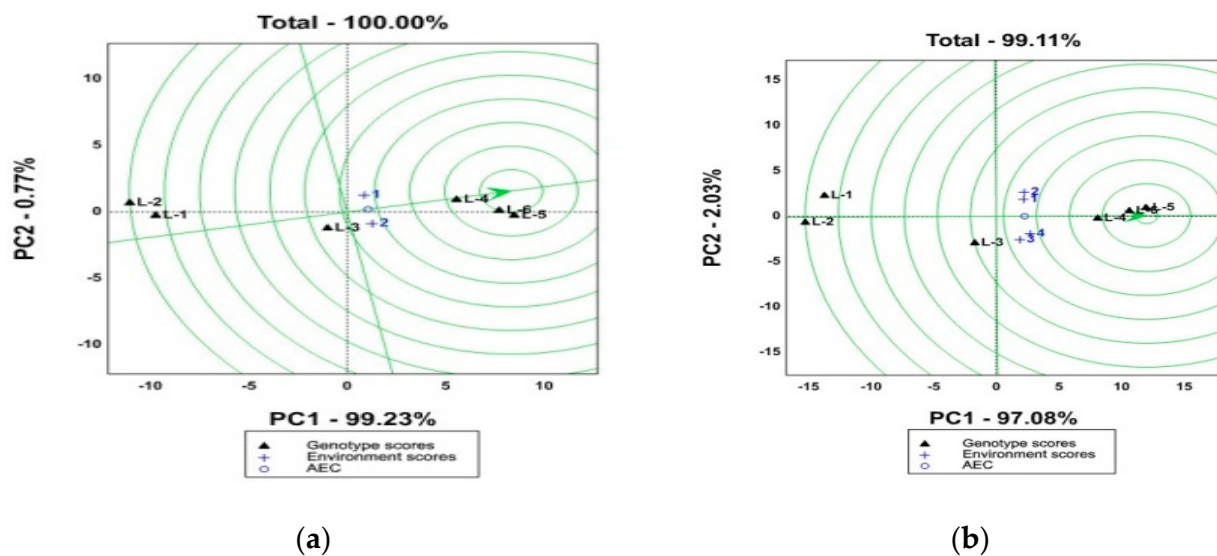

(**a**)   (**b**)

Figure 4. GGE biplot display for the hundred grains weight (g) of maize genotypes according to the ideal genotype model based on the locality, (**a**) and GGE biplot display for the thousand grains weight (g) of maize genotypes according to the ideal genotype model based on the treatment (**b**).

3.7. Correlation Relations between Traits–Spearman's Coefficient

Correlation coefficients obtained on the basis of correlations of the rank of the examined properties are shown in Table 4. High and significant correlations of rank (complete-functional) were observed for the interrelationship of hundred grains weight and yield (1.00).

Table 4. Spermanov coefficient of tested traits.

Parameters	Grain Yield	IPCAG1 (G × Y)	IPCAG1 (G × L)	IPCAG1 (G × T)
HGW	1.000 **	0.600 *	0.257 ns	0.086
GY	-	-	0.086 ns	0.943 **

* and ** significant at 0.05 and 0.01; ns—non significant; GY—grain yield; HGW—hundred grains weight; PCA—principal components analysis; G × Y—Genotype × Year; G × L—Genotype y Locality; G × T—Genotype × Treatment.

When it comes to the correlation coefficients of the rank of the examined traits and IPCAg1 for some interactions that were statistically significant and whose separation by genotypes was realized, it can be stated that it is the influence of genotype and year interaction on hundred grains weight (−0.600 *), and the influence of genotype and treatman interaction on grain yield (−0.943 **),which confirm rank coefficient for IPCAg1 (G × Y) and (G × T) with these properties. This is evidence that the expression of these traits in lines in addition to genotypes is significantly affected by year, treatment and interactions of these factors.

Brankov's results [52] state that from the applied herbicides, sulfonylureas significantly influenced the changes in the content of biochemical parameters in the tested properties of maize genotypes. The average world loss of maize yield, caused by weeds, is estimated to be around 10% [53–56]. Low-grade genotypes PC2 are characterized by broad adaptability, as opposed to specific adaptive genotypes that are located far from the coordinative start. Therefore, the high value of PC2 indicates that the best expression of the trait is in specific agro-ecological conditions [3,4,40].

The GGE biplot method and the AMMI analysis on the basis of which the main components of genotypes and environments, i.e., interactions [57–60], were obtained are of great importance for further research into the stability of maize genotypes [58] and quality [40]. Maize is one of the most abundant cereals on the planet. In Serbia, maize is the most represented crop. Maize is the basis of energy nutrition of domestic animals and significantly affects the competitiveness of beef and milk. In addition to carbohydrates, maize grain contains 5–9% of oils, which are among the highest quality vegetable oils in human nutrition. The hundred grains weight can vary between hybrids, because it depends on agrometeorological conditions, and the amount of applied herbicides and fertilizers. According to the obtained results, genotype G 1 had a higher hundred grains weight than genotype G 2. The hundred grains weight between genotypes did not show statistically significant differences, due to the small difference in the day length of hybrid development. The average of hundred grains weight per genotype G 1 was 375.3 g, and for genotype G 2 it was 365.4 g [11,61].

Cereal productivity is strongly affected by the genetic potential, the growing environment and agricultural practices: genotypes selection [3]; water regimes [13]; nutritional status, especially N utilization [20,45,60], and edaphic and climatic conditions, in particular, temperature changes due to year, location, planting date [17] and application herbicide [3]. The effect of these factors on grain quality is more complex than yield. As an example, apart from interspecies differences, reports have shown that higher N rates reduced rice cooking quality by decreasing amylose [17], and in wheat grain, higher N doses caused an increase in different fractions of proteins and amino acids [18]. Water stress caused an increase in amino acid concentrations of maize grain [23]. As a result, genotype, edaphic and climatic conditions, locality, and application herbicide impact the quantitative characteristics of cereal grains; however, more knowledge is needed on how these factors work in an interactive way [60]. Knowledge of the value of the interaction between the genotype and the external environment is of great importance for more successful breeding work.

4. Conclusions

In the present study, maize genotypes showed relation between traits hundred grains weight and grain yield. The maize genotypes with the highest values of hundred grains weight, such as a L-5 and L-6, expressed the highest values of grain yield (4665 kg/ha and 4445 kg/ha). This indicates that increase in grain yield was closely correlated with increase in the hundred grains weight of maize in both years, which indicates that grain weight was the determining factor influencing variation in maize yield. It provided better insight in the specific association between maize yield trait hundred grains weight of maize, within different localities, treatments and environments. The genotype share in the total phenotypic variance for the trait hundred grains weight was the greatest (64.70%). The share of the year, locality and treatment was 8.42% (4.39% + 3.02% + 1.07%) and the

total interaction was 26.88%. The share of the first IPCA1 for the hundred grains weight in G × T interaction was 50.6% and the share of the second IPCA2 explained about 44.74% of the structures of interaction. Genotype L-6 had the same mass of 100 grains (37.96 g) during both years of testing, while genotype L-1, with 4.46 g, had the largest difference between years. The maize genotype L-5 could be recommended for large-scale production due to high-yielding and stable performance. This clearly indicates the influence of genotype but also stress under the influence of sulfonylureas and environmental factors. By choosing the optimal maize genotype and treatment, it will contribute to the stabilization and increase of maize yield in agroecological conditions of the South Banat Administrative District. Advancefd crop cultivation technology like applied sulfonylureas to achieve high yields grain and resilience plants maize to various biotic and abiotic stresses is of great importace for the food security. Conventional approaches, together with biotechnological tools, aim to increase productivity per maize plant and minimize yield loss at the farmer's level. The collaborative research investments in both approaches are indispensable to food security and sustainable crop maize improvement. Due to great importance, this research should be continued.

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